

AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph [0025] on page 8 with the following amended paragraph:

~~Figure 1~~ FIG. 1 depicts the process of Genetic Reassortment by Mismatch Resolution (GRAMMR). Reassortment is contemplated between two hypothetical polynucleotides differing at at least two nucleotide positions. Annealing between the top strand of A (SEQ ID NO:38; 5'-AGATCGATCAATTG-3') and the bottom strand of B (fully complementary strand of SEQ ID NO:39; SEQ ID NO:39 is 5'-AGACCGATCGATTG-3') is shown (labeled HETERODUPLEX) which results in mismatches at the two positions. After the process of reassortment by mismatch resolution, four distinct product polynucleotides are seen, the parental types A (SEQ ID NO:38 and its fully complementary strand) and B (SEQ ID NO:39 and its fully complementary strand), and the reassorted products [X] C (SEQ ID NO:40; 5'-AGATCGATCGATTG-3' and its fully complementary strand) and [Y] D (SEQ ID NO: 41; 5'-AGACCGATCAATTG-3' and its fully complementary strand).

Please replace the paragraph [0026] on page 8 with the following amended paragraph:

~~Figure 2~~ FIG. 2 depicts an exemplary partially complementary nucleic acid population of two molecules. ~~Figure 2A~~ FIG. 2A shows the sequence of two nucleic acid molecules "X" (SEQ ID NO:36; 5'-AGATCAATTG-3' and its fully complementary strand) and "Y" (SEQ ID NO:37; 5'-AGACCGATTG-3' and its fully complementary strand) having completely complementary top/bottom strands 1+/2- and 3+/4-, respectively. The positions of differing nucleotides between the nucleic acids X and Y are indicated (*). ~~Figure 2B~~ FIG. 2B shows possible combinations of single strands derived from nucleic acids X and Y after denaturing and annealing and indicates which of those combinations would comprise a partially complementary nucleic acid population of two.